

REC'D PCT/PTO PATENT  
13 SEP 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

O. FAMODU ET AL.

CASE NO.: BB1270

APPLICATION NO.: 09/831,683

GROUP ART UNIT: UNKNOWN

INTERNATIONAL FILING DATE: 09 NOV 99 EXAMINER: UNKNOWN

FOR: PLANT AMINOACYL-tRNA SYNTHETASES

STATEMENT UNDER 37 CFR 1.821(g) and 1.825(b)

Assistant Commissioner for Patents  
Washington, DC 20231

Sir:

The submission of the substitute Sequence Listing filed concurrently herewith does not include new matter.

The copy of the substitute Sequence Listing in computer readable form filed concurrently herewith is the same as the paper copy of the substitute Sequence Listing filed concurrently herewith.

Respectfully submitted,



Thomas M. Rizzo, Ph.D.  
Attorney For Applicants  
Registration No. 41,272  
Telephone: 302-892-7760  
Facsimile: 302-892-1026

Dated: August 8, 2001

# SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Aminoacyl-tRNA Synthetases

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 <212> PRT  
 <213> Zea mays

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 Leu Ala Ala Gly Ser Ala Pro Thr Leu Gln Phe Ala Ser Gly Glu Ser  
 35 40 45  
 Leu His Gly Val Asn Pro Ile Ile Leu Tyr Ile Ala Arg Gly Ala Ser  
 50 55 60  
 Ile Ala Ser Leu Ser Gly Lys Asn Asp Ile Glu Phe Gly His Val Val  
 65 70 75 80  
 Glu Trp Leu Glu Tyr Ala Pro Thr Phe Leu Ser Gly Ser Glu Phe Glu  
 85 90 95  
 Asn Ala Cys Leu Phe Val Asp Gly Phe Leu Ala Ser Arg Thr Phe Leu  
 100 105 110  
 Val Gly His Gly Leu Thr Ile Ala Asp Ile Ala Val Trp Ser Asn Leu  
 115 120 125  
 Ala Gly Ile Gly Gln Arg Trp Glu Ser Leu Arg Lys Ser Lys Lys Tyr  
 130 135 140  
 Gln Asn Leu Val Arg Trp Phe Asn Ser Ile Asp Ser Glu Tyr Lys Glu  
 145 150 155 160  
 Ala Leu Asn Glu Val Val Ala Ala Phe Val Gly Lys Arg Gly Ile Gly  
 165 170 175  
 Lys Ser Pro Ala Pro Ser Leu Lys Glu Lys Val His Asp Ser Lys Asp  
 180 185 190  
 Pro Ser Ala Pro Glu Val Asp Leu Pro Gly Ala Lys Val Gly Lys Val  
 195 200 205  
 Cys Val Arg Phe Ala Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His  
 210 215 220  
 Ala Lys Ala Ala Leu Leu Asn Lys Tyr Phe Ala Glu Arg Tyr Gln Gly  
 225 230 235 240  
 Arg Leu Ile Val Arg Phe Asp Asp Thr Asn Pro Ser Lys Glu Ser Asn  
 245 250 255

Glu Phe Val Glu Asn Leu Leu Lys Asp Ile Glu Thr Leu Gly Ile Lys  
 260 265 270  
 Tyr Asp Ala Val Thr Tyr Thr Ser Asp Tyr Phe Pro Lys Leu Met Glu  
 275 280 285  
 Met Ala Glu Ser Leu Ile Lys Gln Gly Lys Ala Tyr Ile Asp Asp Thr  
 290 295 300  
 Pro Lys Glu Gln Met Arg Lys Glu Arg Met Asp Gly Ile Glu Ser Arg  
 305 310 315 320  
 Cys Arg Asn Asn Thr Val Glu Glu Asn Leu Ser Leu Trp Lys Glu Met  
 325 330 335  
 Val Asn Gly Thr Glu Arg Gly Met Gln Cys Cys Val Arg Gly Lys Leu  
 340 345 350  
 Asp Met Gln Asp Pro Asn Lys Ser Leu Arg Asp Pro Val Tyr Tyr Arg  
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 Cys Asn Thr Asp Pro His His Arg Val Gly Ser Lys Tyr Lys Val Tyr  
 370 375 380  
 Pro Thr Tyr Asp Phe Ala Cys Pro Phe Val Asp Ala Leu Glu Gly Val  
 385 390 395 400  
 Thr His Ala Leu Arg Ser Ser Glu Tyr His Asp Arg Asn Ala Gln Tyr  
 405 410 415  
 Tyr Arg Ile Leu Gln Asp Met Gly Leu Arg Arg Val Glu Ile Tyr Glu  
 420 425 430  
 Phe Ser Arg Leu Asn Met Val Tyr Thr Leu Leu Ser Lys Arg Lys Leu  
 435 440 445  
 Leu Trp Phe Val Gln Asn Lys Lys Val Glu Asp Trp Thr Asp Pro Arg  
 450 455 460  
 Phe Pro Thr Val Gln Gly Ile Val Arg Arg Gly Leu Lys Val Glu Ala  
 465 470 475 480  
 Leu Ile Gln Phe Ile Leu Gln Gln Gly Ala Ser Lys Asn Leu Asn Leu  
 485 490 495  
 Met Glu Trp Asp Lys Leu Trp Thr Ile Asn Lys Lys Ile Ile Asp Pro  
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 Val Cys Ala Arg His Thr Ala Val Leu Lys Asp Gln Arg Val Ile Phe  
 515 520 525  
 Thr Leu Thr Asn Gly Pro Glu Glu Pro Phe Val Arg Ile Leu Pro Arg  
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 His Lys Lys Phe Glu Gly Ala Gly Lys Lys Ala Thr Thr Phe Ala Asn  
 545 550 555 560  
 Arg Ile Trp Leu Asp Tyr Ala Asp Ala Ala Ala Ile Asn Lys Gly Glu  
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Glu Val Thr Leu Met Asp Trp Gly Asn Ala Ile Val Lys Glu Ile Lys  
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 595 600 605  
 Gly Ser Val Lys Thr Thr Lys Leu Lys Ile Thr Trp Leu Ala Asp Ile  
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 Glu Glu Leu Val Pro Leu Ser Leu Val Glu Phe Asp Tyr Leu Ile Ser  
 625 630 635 640  
 Lys Lys Lys Leu Glu Glu Asp Glu Asp Phe Leu Asp Asn Leu Asn Pro  
 645 650 655  
 Cys Thr Arg Arg Glu Ile Pro Ala Leu Gly Asp Ala Asn Met Arg Asn  
 660 665 670  
 Ile Lys Arg Gly Glu Ile Ile Gln Leu Glu Arg Lys Gly Tyr Tyr Arg  
 675 680 685  
 Cys Asp Ala Pro Phe Ile Arg Ser Ser Lys Pro Val Val Leu Phe Ala  
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 <212> DNA  
 <213> Oryza sativa

<220>  
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 <222> (139)

<220>  
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 <222> (238)

<220>  
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 <222> (431)

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 tggccagcca gtgtataact tctgtgtcac agttgatgat gctaccatgc gcattctctca 780  
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 <211> 555  
 <212> PRT  
 <213> *Oryza sativa*

<220>  
 <221> UNSURE  
 <222> (130)

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 His Arg Thr Ala Pro Ala Ala Arg Cys Gly Pro Val Arg Ala Val Ala  
 35 40 45  
 Asp Gly Asn Leu His Val Gly Gly Ala Arg Thr Ala His Phe Asn Tyr  
 50 55 60  
 Leu Phe Ala Arg Ser Lys Gly Gly Lys Phe Val Leu Arg Ile Glu Asp  
 65 70 75 80  
 Thr Asp Phe Glu Arg Ser Thr Lys Lys Ser Glu Glu Ala Val Leu Ser  
 85 90 95  
 Asp Leu Ala Trp Leu Gly Leu Asp Trp Asp Glu Gly Pro Asp Val Gly  
 100 105 110  
 Gly Glu Tyr Gly Pro Asp Arg Gln Ser Glu Arg Asn Ser Met Tyr Lys  
 115 120 125  
 Gln Xaa Ala Glu Lys Leu Met Glu Ser Gly Ala Val Tyr Gln Cys Phe  
 130 135 140  
 Tyr Ser Ser Glu Gly Leu Glu Gln Met Lys Glu Thr Ala Ser Arg Cys  
 145 150 155 160  
 Asn Leu Pro Pro Val Tyr Ile Gly Lys Trp Gly Thr Ala Ser Asp Ala  
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Glu	Ile	Gln	Gln	Glu	Leu	Glu	Lys	Gly	Thr	Pro	Tyr	Thr	Tyr	Arg	Phe		
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Ser	Asn	Gly	Gln	Pro	Val	Tyr	Asn	Phe	Cys	Val	Thr	Val	Asp	Asp	Ala		
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Thr	Leu	Arg	Gln	Ala	Leu	Ile	Tyr	Lys	Ala	Leu	Gly	Phe	Pro	Met	Pro		
			260					265					270				
Ser	Phe	Ala	His	Val	Ser	Leu	Ile	Leu	Ala	Pro	Asp	Arg	Ser	Lys	Leu		
	275						280					285					
Ser	Lys	Arg	His	Gly	Ala	Thr	Ser	Val	Gly	Gln	Tyr	Lys	Glu	Met	Gly		
	290					295					300						
Tyr	Leu	Pro	Gln	Ala	Met	Val	Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Gly		
305					310					315					320		
Asp	Gly	Thr	Glu	Asn	Glu	Phe	Phe	Thr	Ile	Asp	Asp	Leu	Val	Glu	Lys		
				325					330					335			
Phe	Thr	Ile	Asn	Arg	Val	Asn	Lys	Ser	Gly	Ala	Val	Phe	Asp	Ala	Val		
			340				345						350				
Lys	Leu	Lys	Trp	Met	Asn	Gly	Gln	His	Leu	Arg	Ser	Phe	Pro	Pro	Asp		
		355					360					365					
Val	Leu	Ile	Lys	Ser	Phe	Glu	Asp	Arg	Trp	Lys	Asp	Thr	Gly	Ile	Leu		
	370					375					380						
Gln	Glu	Ser	Glu	Ser	Gly	Phe	Ala	Lys	Glu	Ala	Ala	Glu	Leu	Leu	Lys		
385					390					395					400		
Asp	Gly	Ile	Asp	Leu	Ile	Thr	Asp	Ala	Asp	Ala	Ala	Leu	Ser	Asn	Leu		
				405				410						415			
Leu	Ser	Tyr	Pro	Leu	His	Ala	Thr	Leu	Ser	Ser	Asp	Glu	Ala	Lys	Ser		
			420					425					430				
Val	Val	Gln	Asp	Lys	Leu	Ser	Glu	Val	Ala	Ser	Gly	Leu	Ile	Ser	Ala		
		435					440					445					
Tyr	Asp	Ser	Gly	Glu	Leu	Cys	Gln	Ala	Leu	Ala	Glu	Gly	Arg	Asp	Gly		
	450					455					460						
Trp	Gln	Lys	Trp	Val	Lys	Ile	Phe	Gly	Lys	Ser	Leu	Lys	Arg	Lys	Gly		
465					470					475					480		
Lys	Ser	Leu	Phe	Met	Pro	Leu	Arg	Val	Leu	Leu	Thr	Gly	Lys	Leu	His		
				485					490					495			

Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys Ala Gly Thr  
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Cys Gly Ala Val Thr Gln Gln Ser Gly Phe Val Asn Leu Asp Glu Arg  
515 520 525

Phe Arg Ile Leu Lys Glu Val Glu Trp Glu Ser Leu Val Gln Glu Gln  
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Glu Ser Pro Ala Glu Thr Ala Val Pro Ala Ser  
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<211> 731  
<212> DNA  
<213> Glycine max

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tttctcaagt ctctgctctc tccgaacaac caccacccgt tcgcgttcgt ttcgctcctt 180  
ctcccaccgg aaacctccac gtcggcgggtg cccgaacggc cctcttcaac tacttggttcg 240  
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caggtaaattg ggccagtgc acaaatgagg aagtagaaga agagctagca aaaggaactc 600  
cttacactta ccggttccga gtccctaaag gaagtttaaa aattaatgat caaatacgag 660  
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agcctgttta t 731

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<211> 404  
<212> PRT  
<213> Glycine max

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Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Ser Thr  
35 40 45  
Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
50 55 60  
Asp Trp Asp Glu Gly Pro Gly Val Gly Gly Asp Tyr Gly Pro Tyr Arg  
65 70 75 80  
Gln Ser Asp Arg Asn Ser Leu Tyr Lys Gln Phe Ala Asp Asn Leu His  
85 90 95  
Gln Ser Gly His Val Tyr Arg Cys Phe Cys Ser Asn Glu Glu Leu Glu  
100 105 110

Lys Met Lys Glu Asp Ala Lys Leu Lys Gln Leu Pro Pro Val Tyr Thr  
 115 120 125  
 Gly Lys Trp Ala Ser Ala Thr Asn Glu Glu Val Glu Glu Glu Leu Ala  
 130 135 140  
 Lys Gly Thr Pro Tyr Thr Tyr Arg Phe Arg Val Pro Lys Gly Ser Leu  
 145 150 155 160  
 Lys Ile Asn Asp Gln Ile Arg Gly Glu Val Ser Trp Asn Leu Asp Thr  
 165 170 175  
 Leu Gly Asp Phe Val Ile Met Arg Ser Asn Gly Gln Pro Val Tyr Asn  
 180 185 190  
 Phe Cys Val Thr Val Asp Asp Ala Thr Met Ala Ile Ser His Val Ile  
 195 200 205  
 Arg Ala Glu Glu His Leu Pro Asn Thr Leu Arg Gln Ala Leu Ile Tyr  
 210 215 220  
 Lys Ala Leu Gly Phe Pro Met Pro His Phe Ala His Val Ser Leu Ile  
 225 230 235 240  
 Leu Ala Pro Asp Arg Ser Lys Leu Ser Lys Arg His Gly Ala Thr Ser  
 245 250 255  
 Val Gly Gln Phe Arg Asp Met Gly Tyr Leu Pro Gln Ala Met Val Asn  
 260 265 270  
 Tyr Leu Ala Leu Leu Gly Trp Gly Asp Gly Thr Glu Asn Glu Phe Phe  
 275 280 285  
 Thr Leu Glu Gln Leu Val Glu Lys Phe Thr Ile Glu Arg Val Asn Lys  
 290 295 300  
 Ser Gly Ala Ile Phe Asp Ser Thr Lys Leu Arg Trp Met Asn Gly Gln  
 305 310 315 320  
 His Leu Arg Ser Leu Pro Ser Glu Glu Leu Asn Arg Ile Ile Gly Glu  
 325 330 335  
 Arg Trp Lys Asp Ala Gly Ile Ala Thr Glu Ser Gln Gly Ile Phe Ile  
 340 345 350  
 Gln Asp Ala Val Leu Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp  
 355 360 365  
 Ser Glu Lys Ala Leu Ser Ser Leu Leu Ser Tyr Pro Leu Tyr Glu Thr  
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 Val Ala Lys Ser

<210> 15  
 <211> 407



<212> DNA  
<213> Triticum aestivum

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<222> (14)

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gccctcttca attacctgat tgcaaaaagct acacgcggta aattcatcct acgcatagag 240  
gacacagatn agtcaaggac tgttcctggt gcgattgaaa aactctgcgc tgntttgaga 300  
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<212> PRT  
<213> Triticum aestivum

<220>  
<221> UNSURE  
<222> (55)

<220>  
<221> UNSURE  
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Ala Pro Ser Pro Thr Gly Asn Leu His Leu Gly Ser Leu Arg Thr Ala  
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Leu Phe Asn Tyr Leu Ile Ala Lys Ala Thr Arg Gly Lys Phe Ile Leu  
35 40 45

Arg Ile Glu Asp Thr Asp Xaa Ser Arg Thr Val Pro Gly Ala Ile Glu  
50 55 60

Lys Leu Cys Ala Xaa Leu Arg Trp Gly Gly Leu Lys Arg Asp Lys  
65 70 75

<210> 17  
<211> 2387  
<212> DNA  
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<400> 17

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tcgaatcccc	tgagtcccaa	tgcattatgc	tgatgaatca	ggctgcagac	atattgtgaa	2340
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<210> 18  
 <211> 495  
 <212> PRT  
 <213> Zea mays

<400> 18

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Asn	Ser	Ala	Ser	Val	Ala	Glu	Trp	Ala	Thr	Ser	Leu	Ser	Leu	Leu	Phe
			20					25					30		
Asp	Pro	Lys	Cys	Pro	Gly	Leu	Glu	Ser	Leu	Val	Glu	Lys	Val	Lys	Glu
		35					40					45			
Ile	Val	Glu	Ser	Asn	Glu	Val	Arg	Arg	Leu	Pro	Lys	Ile	Pro	Lys	Gly
	50					55					60				
Thr	Arg	Asp	Phe	Gly	Lys	Glu	Gln	Met	Ala	Ile	Arg	Glu	Arg	Ala	Phe
	65				70					75					80
Ser	Ile	Ile	Thr	Ser	Val	Phe	Lys	Met	His	Gly	Ala	Thr	Ala	Leu	Asp
				85					90					95	
Thr	Pro	Val	Phe	Glu	Leu	Arg	Glu	Thr	Leu	Met	Gly	Lys	Tyr	Gly	Glu
			100					105					110		
Asp	Ser	Lys	Leu	Ile	Tyr	Asp	Leu	Ala	Asp	Gln	Gly	Gly	Glu	Leu	Cys
		115					120					125			
Ser	Leu	Arg	Tyr	Asp	Leu	Thr	Val	Pro	Phe	Ala	Arg	Tyr	Val	Ala	Met
	130					135						140			
Asn	Ser	Ile	Ser	Ala	Leu	Lys	Arg	Tyr	Gln	Ile	Ala	Lys	Val	Tyr	Arg
145					150					155					160
Arg	Asp	Asn	Pro	Ser	Lys	Gly	Arg	Tyr	Arg	Glu	Phe	Tyr	Gln	Cys	Asp
				165					170					175	
Phe	Asp	Ile	Ala	Gly	Val	Tyr	Glu	Pro	Met	Glu	Pro	Asp	Phe	Glu	Val
			180					185					190		
Ile	Lys	Val	Leu	Thr	Glu	Leu	Leu	Asn	Gln	Leu	Asp	Ile	Gly	Thr	Tyr
		195					200					205			
Glu	Ile	Lys	Leu	Asn	His	Arg	Lys	Leu	Leu	Asp	Gly	Met	Leu	Glu	Ile
	210					215					220				
Cys	Gly	Val	Pro	Pro	Gln	Lys	Phe	Arg	Thr	Val	Cys	Ser	Ser	Ile	Asp
225					230					235					240
Lys	Leu	Asp	Lys	Gln	Thr	Phe	Glu	Gln	Val	Lys	Lys	Glu	Leu	Val	Asp
				245					250					255	
Glu	Lys	Gly	Ile	Ser	Asn	Glu	Thr	Ala	Asp	Glu	Ile	Gly	Asn	Leu	Val
			260					265					270		
Lys	Thr	Arg	Gly	Pro	Pro	Leu	Glu	Val	Leu	Met	Glu	Leu	Arg	Lys	Glu
		275					280					285			



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 <222> (740)

<400> 19  
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 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180  
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
 tgaaagctgt tggctctatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
 agtcattgac cgagttagaa gagagacttg ggagcagtg ggaagcagtt gctgatctga 360  
 aacagctatt ctcccttgct gaaaaaattg gttactctaa atggcttcaa tttgatgcat 420  
 cagttgttcg aggtcttgct tactacactg gcattgtatt tgagggtttt gaccgagaag 480  
 gaaagctgag agctatctgt ggtggtggc gatatgatca tttgttctca acttttgggtg 540  
 ctgatgacat tgctgcatgt ggttttggat ttggtgatgc aagtcatagt ggaattgctc 600  
 aaaagagaan ggtctgttac cgggaagctt aacttgcaaa tagatgacat tgtgtgtgcc 660  
 ttggaccaaa gatcttcaag ggatgtgctg ctatgggccc caacaatctc agngaaaaan 720  
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 <211> 243  
 <212> PRT  
 <213> Glycine max

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 <222> (203)

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 <222> (235)

<220>  
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 <222> (238)

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 20 25 30  
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
 35 40 45  
 Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 50 55 60  
 Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 65 70 75 80  
 Lys Ala Val Gly Leu Ser Gln Glu Ala Val Gln Glu Leu Leu Gln Val  
 85 90 95

Leu Ser Val Lys Ser Leu Thr Glu Leu Glu Glu Arg Leu Gly Ser Ser  
 100 105 110  
 Gly Glu Ala Val Ala Asp Leu Lys Gln Leu Phe Ser Leu Ala Glu Lys  
 115 120 125  
 Ile Gly Tyr Ser Lys Trp Leu Gln Phe Asp Ala Ser Val Val Arg Gly  
 130 135 140  
 Leu Ala Tyr Tyr Thr Gly Ile Val Phe Glu Gly Phe Asp Arg Glu Gly  
 145 150 155 160  
 Lys Leu Arg Ala Ile Cys Gly Gly Gly Arg Tyr Asp His Leu Phe Ser  
 165 170 175  
 Thr Phe Gly Ala Asp Asp Ile Ala Ala Cys Gly Phe Gly Phe Gly Asp  
 180 185 190  
 Ala Ser His Ser Gly Ile Ala Gln Lys Arg Xaa Val Cys Tyr Arg Glu  
 195 200 205  
 Ala Leu Ala Asn Arg His Cys Val Cys Leu Gly Pro Lys Ile Phe Lys  
 210 215 220  
 Gly Cys Ala Ala Met Gly Pro Asn Asn Leu Xaa Glu Lys Xaa Gln Ile  
 225 230 235 240  
 Val Glu Val

<210> 21  
 <211> 1164  
 <212> DNA  
 <213> Triticum aestivum

<400> 21  
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 tgacaagctg gggaaactga gtagggaaga aattgagaag gaattgattt caactgggct 180  
 gtcactctgaa gcagtacagg gcatcattga agtgctctct ctcaagtcac tgtccaaact 240  
 tgaagaggtg ctaggctcag gtgttgaagc cgttgctgac ttgaagaagc tcttctcgct 300  
 tgctgagcaa tatggttatt ctgattggat ctgtttcgat gcatctgttg ttcgtggcct 360  
 tgcatactac acagggattg tttttgaggc ttttgatagg gaaggggaac tgagagcgat 420  
 ttgtggtggg gggagggtatg acaggctact gtcaacattt ggaactgaag atgtaccagc 480  
 ctgtggcttt ggatttggag atgctgtcat agtggagctg ctgaaagaaa agggctcttt 540  
 gcctgacctg ccacgtcaaa tagatgacat tgtgttccca ttggacgagg agcttgaggg 600  
 gccagcatct agtgttgcat cctgtctgag gaagaaggcg agatctgtag accttgtaga 660  
 agacaagcgt ctgaaatggg tgttcaaaca tgctgagagg ataaacgcta gcaggctgat 720  
 cttggttggg aaatccgagt gggagcagag catggtccgt gtgaagatac tatcaaccag 780  
 agaagagttc gaggtcaagg cgggcgaatt gcagtagctg ttagctgatc tggctcgattt 840  
 gaaggtttga cttgtcccct ttcttctttc tgatcatctt caaactgtga agttttgcaa 900  
 ttcacgtcgt gtatacaaac aattaggtgg ctttgaatgc tattgccatc ttctttcgga 960  
 tcattcacct tgcaacaaac aaagaaattg taggttttgc cattcaccaa catgtattga 1020  
 gaatgcctt gctgcctgag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080  
 aaaaaaaaaa aaaaaaaaaa aaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1140  
 aaaaaaaaaa aaaaaaaaaa aaaa 1164

<210> 22  
 <211> 271

<212> PRT  
 <213> Triticum aestivum

<400> 22

Lys	Leu	Gly	Ile	Thr	Ser	Ser	Asp	Val	Gly	Ile	Arg	Leu	Ser	Ser	Arg	1	5	10	15
Lys	Val	Leu	Gln	Ala	Val	Leu	Asp	Met	Tyr	Ser	Val	Pro	Gln	His	Leu	20	25	30	
Phe	Thr	Gln	Val	Cys	Val	Ile	Val	Asp	Lys	Leu	Gly	Lys	Leu	Ser	Arg	35	40	45	
Glu	Glu	Ile	Glu	Lys	Glu	Leu	Ile	Ser	Thr	Gly	Leu	Ser	Ser	Glu	Ala	50	55	60	
Val	Gln	Gly	Ile	Ile	Glu	Val	Leu	Ser	Leu	Lys	Ser	Leu	Ser	Lys	Leu	65	70	75	80
Glu	Glu	Val	Leu	Gly	Ser	Gly	Val	Glu	Ala	Val	Ala	Asp	Leu	Lys	Lys	85	90	95	
Leu	Phe	Ser	Leu	Ala	Glu	Gln	Tyr	Gly	Tyr	Ser	Asp	Trp	Ile	Cys	Phe	100	105	110	
Asp	Ala	Ser	Val	Val	Arg	Gly	Leu	Ala	Tyr	Tyr	Thr	Gly	Ile	Val	Phe	115	120	125	
Glu	Ala	Phe	Asp	Arg	Glu	Gly	Glu	Leu	Arg	Ala	Ile	Cys	Gly	Gly	Gly	130	135	140	
Arg	Tyr	Asp	Arg	Leu	Leu	Ser	Thr	Phe	Gly	Thr	Glu	Asp	Val	Pro	Ala	145	150	155	160
Cys	Gly	Phe	Gly	Phe	Gly	Asp	Ala	Val	Ile	Val	Glu	Leu	Leu	Lys	Glu	165	170	175	
Lys	Gly	Leu	Leu	Pro	Asp	Leu	Pro	Arg	Gln	Ile	Asp	Asp	Ile	Val	Phe	180	185	190	
Pro	Leu	Asp	Glu	Glu	Leu	Glu	Gly	Pro	Ala	Ser	Ser	Val	Ala	Ser	Cys	195	200	205	
Leu	Arg	Lys	Lys	Gly	Arg	Ser	Val	Asp	Leu	Val	Glu	Asp	Lys	Arg	Leu	210	215	220	
Lys	Trp	Val	Phe	Lys	His	Ala	Glu	Arg	Ile	Asn	Ala	Ser	Arg	Leu	Ile	225	230	235	240
Leu	Val	Gly	Lys	Ser	Glu	Trp	Glu	Arg	Gly	Met	Val	Arg	Val	Lys	Ile	245	250	255	
Leu	Ser	Thr	Arg	Glu	Glu	Phe	Glu	Val	Lys	Ala	Gly	Glu	Leu	Gln	260	265	270		

<210> 23  
 <211> 913  
 <212> DNA  
 <213> Zea mays

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 aggagagtga ggggtgccga gtttatatta ttcaagggtca tcaaateccct ttgattgttg 120  
 ttaagagtga tgggtggcttc aactatgcct caacagactt aactgctctt tggatcggc 180  
 tcaatgttga gcaggcagag tggatcatat atgttacaga tgttggtcag cagcagcact 240  
 ttgacatggt tttcagtgcg gcaaagatgg ccggttggtc cccagatcca agtgaaaaga 300  
 agttttccgaa aacaagccat gttggatttg gtcttgttct tggttcaaga tggcaagcgg 360  
 ttccgaaccc gcagtactga ggttggttga ttggtagagc tacttgatga ggctaaatct 420  
 cggagcaaat cagaactact acaacggctc actgaaaatg gcaaaattgt tgactggacg 480  
 gatgangaat tagagcaaac ttcagaggct gttggatatg gtgctgtgaa gtacgctgat 540  
 ctaaaaaata acaggctcac taattacaca tttagttttg aacaaatgct gagcgataag 600  
 ggaaatactg ctgtgtacct tcagtatgca catgctcgta tttgttccat tattcggaaa 660  
 tccaacaaga acgtggnaga ctgaagagat ggagccatct ctctcgacca tccggattag 720  
 cgctgttggg gctgtatctt anccgatttg cagagttggt gaagaggatc acgaactact 780  
 ccaaatttgt gtgtgaatac tgtcaatcan ctgaaagtca caanatcata caactgcaag 840  
 tgggtgggtcc ngaggaacac cgggtgtgctt gcaacgacgc gtttcacna agnctcaccg 900  
 ctcggatacn cat 913

<210> 24  
 <211> 221  
 <212> PRT  
 <213> Zea mays



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 <222> (96)

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<220>  
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<400> 24

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 1 5 10 15

Gly Leu Ile Lys Glu Ser Glu Gly Ala Arg Val Ile Phe Ile Gln Gly  
 20 25 30

His Gln Ile Pro Leu Ile Val Val Lys Ser Asp Gly Gly Phe Asn Tyr  
 35 40 45

Ala Ser Thr Asp Leu Thr Ala Leu Trp Tyr Arg Leu Asn Val Glu Gln  
 50 55 60

Ala Glu Trp Ile Ile Tyr Val Thr Asp Val Gly Gln Gln Gln His Phe  
 65 70 75 80

Asp Met Val Phe Ser Ala Ala Lys Met Ala Gly Trp Leu Pro Asp Xaa  
 85 90 95

Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Phe Leu  
 100 105 110

Val Gln Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
 115 120 125

Leu Val Glu Leu Leu Asp Glu Ala Lys Ser Arg Ser Lys Ser Glu Leu  
 130 135 140

Thr Glu Asn Gly Lys Ile Val Asp Trp Thr Asp Xaa Glu Leu Glu Gln  
 145 150 155 160

Thr Ser Glu Ala Val Gly Tyr Gly Ala Val Lys Tyr Ala Asp Leu Lys  
 165 170 175

Asn Asn Arg Leu Thr Asn Tyr Thr Phe Ser Phe Glu Gln Met Leu Ser  
 180 185 190

Asp Lys Gly Asn Thr Ala Val Tyr Leu Gln Tyr Ala His Ala Arg Ile  
 195 200 205

Cys Ser Ile Ile Arg Lys Ser Asn Lys Asn Val Xaa Asp  
 210 215 220

<210> 25  
 <211> 551  
 <212> DNA  
 <213> Oryza sp.

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 tccctgcgtg caacagtacc tgacctggat gtggaaccga tgcttgaagt ctcaaaacca 120  
 ggttttgggg attaccagtg caacaatgct atgagtgtat tttcaagaat aagaggatcc 180  
 gcaacaaact tccgtaaccc catggcagtt gggcaggcaa ttgcaaataa cctccccag 240  
 tcaaataatta tcgaatccat ctctgttgcc ggancgtggt acattaacat aacgttatcc 300  
 agcaattgga ttgcacagag gatacaaaga catgcttggt tgtgggaatc aaaacatggg 360  
 gaacaatcct taacctgttt aagaaggcaa ntgctggntt tttcaanccc caataattgc 420  
 aaaaagaana tgcaagttgg gcaataatna aggncaacaa taaatngggg natancccaa 480  
 ctcaaaaangg ttgnggntca caaaanggtt aanttcntcn acgtaaacan gttgggaaac 540  
 nggggnacac a 551

<210> 26  
 <211> 68  
 <212> PRT  
 <213> Oryza sp.

<220>  
 <221> UNSURE  
 <222> (51)

<400> 26  
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 Arg Gly Ser Ala Thr Asn Phe Arg Asn Pro Met Ala Val Gly Gln Ala  
 20 25 30  
 Ile Ala Asn Asn Leu Pro Gln Ser Asn Ile Ile Glu Ser Ile Ser Val  
 35 40 45  
 Ala Gly Xaa Gly Tyr Ile Asn Ile Thr Leu Ser Ser Asn Trp Ile Ala  
 50 55 60  
 Gln Arg Ile Gln  
 65

<210> 27  
 <211> 411

<212> DNA  
<213> Glycine max

<220>  
<221> unsure  
<222> (18)

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<400> 27  
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acaactgatc tagcatcact ttggtatcgt ctaaataaag aaaaacttga atggattgta 120  
tatgttacag atattgggca gcaacagcac tttgatatnc tattnaaggc ctataggcgt 180  
gcaggttggt taccaaagga tgagaatgcg tatccaaaat gtactcatat aggttttggt 240  
cttggtcttg gggaagatgg aaaacgattt cggactcgca ncagtnangt tgttcgatta 300  
gttgattact tgatgaagct aaaangcgt gtaaaattgc cntcttgaaa cgtgatacaa 360  
ctaaaggatt ggnctgaagg aggagatcga gaaaacatcc gaagcagttg g 411

<210> 28  
<211> 115  
<212> PRT  
<213> Glycine max

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<222> (6)

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<400> 28  
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Xaa Asn Tyr Phe Thr Thr Asp Leu Ala Ser Leu Trp Tyr Arg Leu Asn  
20 25 30  
Glu Glu Lys Leu Glu Trp Ile Val Tyr Val Thr Asp Ile Gly Gln Gln  
35 40 45  
Gln His Phe Asp Xaa Leu Xaa Lys Ala Tyr Arg Arg Ala Gly Trp Leu  
50 55 60  
Pro Lys Asp Glu Asn Ala Tyr Pro Lys Cys Thr His Ile Gly Phe Gly  
65 70 75 80  
Leu Val Leu Gly Glu Asp Gly Lys Arg Phe Arg Thr Arg Xaa Ser Xaa  
85 90 95  
Val Val Arg Leu Val Asp Tyr Leu Met Lys Leu Lys Xaa Ala Val Lys  
100 105 110  
Leu Pro Ser  
115

<210> 29  
<211> 565

<212> DNA  
<213> Triticum sp.

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<222> (555)

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caaaaacgag tcatgttggg tttggccttg ttcttggagc agatggcaag cgcttccgaa 120  
ctcgtagtagt tgaggttggt cggttgggaa gacctacttg atgaggctaa atctcgaagt 180  
aaatcaagaa cttctccaag cgtctcactg gaaaatggta aaattgttga ctggactgat 240  
gaaggaacta agagcaaact tcaaaaggca gtaagatatg gcgctgtcaa agtatgcggg 300  
tctgaaagaa taaccgactg actaattaca cttcaacttt gattcaagan ctaagtgaca 360  
agggaaatac tgctgtcnac ttcaataagc caagcccgtg cctcccanca ttcnaaaacc 420  
caacatgggtg tnnaaaacta aaangatggg anattccncc tgccanccaa atagctgcct 480  
gggacgnact aacngtatgc aanatgttaa aaggatgaca acncttccaa tgtcngggng 540  
aaactatnac tacnaagta aaagt 565

<210> 30  
<211> 33  
<212> PRT  
<213> Triticum sp.

<400> 30  
Glu Lys Lys Phe Pro Lys Thr Ser His Val Gly Phe Gly Leu Val Leu  
1 5 10 15  
Gly Ala Asp Gly Lys Arg Phe Arg Thr Arg Ser Thr Glu Val Val Arg  
20 25 30

Leu

<210> 31  
<211> 546  
<212> DNA  
<213> Oryza sp.

<220>  
<221> unsure  
<222> (448)

<220>  
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<222> (512)

<400> 31  
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cattctccag gagtctgaaa gtggttttgc taaagaagcg gctgagcttt tgaaggatgg 120  
catcgatttg atcactgatg ctgacgcagc cctttcaaac ctgttgcgt atccctccca 180

tgctacatta agcagtgatg aagctaaatc tgtgggtgcaa gacaagcttt ctgaggttgc 240  
 atcaggactc atttctgctt atgatatcgg tgaactttgt caagcactag ctgagggccg 300  
 tgatgggttg cagaagtggg tgaataatct tggcaaatca cttaaaagaa agggaaaagtc 360  
 actctttatg ccgctccgtg tactgctgac tggcaagctt catgggcctg acatgggcgg 420  
 caccgtagtc ctcatacaca aagccggnac tgtggagcgg tcactcaaca atccgggttc 480  
 gtaaactctg acgagaggtc agaatcctga angagtggag tggagtcact ggtacaggac 540  
 aagatc 546

<210> 32  
 <211> 147  
 <212> PRT  
 <213> Oryza sp.

<400> 32  
 Pro Pro Asp Val Leu Ile Lys Ser Phe Glu Asp Arg Trp Lys Asp Thr  
 1 5 10 15  
 Gly Ile Leu Gln Glu Ser Glu Ser Gly Phe Ala Lys Glu Ala Ala Glu  
 20 25 30  
 Leu Leu Lys Asp Gly Ile Asp Leu Ile Thr Asp Ala Asp Ala Ala Leu  
 35 40 45  
 Ser Asn Leu Leu Ser Tyr Pro Leu His Ala Thr Leu Ser Ser Asp Glu  
 50 55 60  
 Ala Lys Ser Val Val Gln Asp Lys Leu Ser Glu Val Ala Ser Gly Leu  
 65 70 75 80  
 Ile Ser Ala Tyr Asp Ser Gly Glu Leu Cys Gln Ala Leu Ala Glu Gly  
 85 90 95  
 Arg Asp Gly Trp Gln Lys Trp Val Lys Ile Phe Gly Lys Ser Leu Lys  
 100 105 110  
 Arg Lys Gly Lys Ser Leu Phe Met Pro Leu Arg Val Leu Leu Thr Gly  
 115 120 125  
 Lys Leu His Gly Pro Asp Met Gly Gly Thr Val Val Leu Ile His Lys  
 130 135 140  
 Ala Gly Thr  
 145

<210> 33  
 <211> 524  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (386)

<220>  
 <221> unsure  
 <222> (423)

<220>  
 <221> unsure  
 <222> (459)



<220>  
 <221> unsure  
 <222> (481)

<220>  
 <221> unsure  
 <222> (483)

<220>  
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 <222> (486)

<400> 33  
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 accactctca caccctctgc acctttcttct tccaacgacg ccgtttctca gtctctgctc 120  
 tctccgaaca accaccaccc gtctcggttc gtttcgctcc ttctcccacc ggaaacctcc 180  
 acgtcggcgg tgcccgaacg gccctcttca actacttggt cgcaagggtcc aaagggtggga 240  
 aatttgtgct gagaattgag gacactgact tggagaggtc caagtaggga gtctgaggag 300  
 gccatgctca aagatctttc ttggcttggc cttgattggg atgaagggcc tgggtgttgg 360  
 aggggattat ggtccttaaa aggcantctg agaaggaatt ccttatacaa acaatatgcc 420  
 ggnгаааacta cacaaatccg ggcaagttta accgctgcnt tctggtccaa agagggaact 480  
 nanagnaaat gaaaggaggt tgctaaacta aagcaactgg cccc 524

<210> 34  
 <211> 94  
 <212> PRT  
 <213> Glycine max

<220>  
 <221> UNSURE  
 <222> (63)

<400> 34  
 Gln Arg Arg Arg Phe Ser Val Ser Ala Leu Ser Glu Gln Pro Pro Pro  
 1 5 10 15  
 Val Arg Val Arg Phe Ala Pro Ser Pro Thr Gly Asn Leu His Val Gly  
 20 25 30  
 Gly Ala Arg Thr Ala Leu Phe Asn Tyr Leu Phe Ala Arg Ser Lys Gly  
 35 40 45  
 Gly Lys Phe Val Leu Arg Ile Glu Asp Thr Asp Leu Glu Arg Xaa Ser  
 50 55 60  
 Arg Glu Ser Glu Glu Ala Met Leu Lys Asp Leu Ser Trp Leu Gly Leu  
 65 70 75 80  
 Asp Trp Asp Lys Gly Leu Gly Val Gly Gly Asp Tyr Gly Pro  
 85 90

<210> 35  
 <211> 506  
 <212> DNA  
 <213> Glycine max

<220>  
 <221> unsure  
 <222> (18)

<220>  
 <221> unsure  
 <222> (483)

<220>  
 <221> unsure  
 <222> (505)

<220>  
 <221> unsure  
 <222> (506)

<400> 35  
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 tcgtcacttt gtttaagcga ataggaatta cagaatcaga tgtcggattt aagggttcca 120  
 gtcgaaaggt tctgcaagaa gtattaaatt gttattcagt accagaaaat ttatttggca 180  
 aggtctgcgt cattattgat aaaattgaga aaattccagc tgacgagata aagaaagagt 240  
 tgaaagctgt tggcttatct caagaggctg tccaggagct attgcaagtc ctttctgtga 300  
 agtcattgac cgagttagaa gagagacttg ggagagtggg gaagcagttg ctgatctgaa 360  
 acagtattct cccttgctga aaaaattggt tactctaaat gggtcaattt gatgatagtt 420  
 gttcgaggtc ttgcttacta cactggcatt gatttgaggg tttgacgaga ggaagctgca 480  
 gcntctgtgt gtgtcaatac attgnn 506

<210> 36  
 <211> 48  
 <212> PRT  
 <213> Glycine max

<400> 36  
 Asp Val Gly Phe Lys Val Ser Ser Arg Lys Val Leu Gln Glu Val Leu  
 1 5 10 15

Asn Cys Tyr Ser Val Pro Glu Asn Leu Phe Gly Lys Val Cys Val Ile  
 20 25 30

Ile Asp Lys Ile Glu Lys Ile Pro Ala Asp Glu Ile Lys Lys Glu Leu  
 35 40 45

<210> 37  
 <211> 577  
 <212> DNA  
 <213> Triticum sp.

<220>  
 <221> unsure  
 <222> (140)

<220>  
 <221> unsure  
 <222> (370)

<220>  
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 <222> (411)

<220>  
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<220>  
 <221> unsure  
 <222> (469)

<220>  
 <221> unsure  
 <222> (481)

<220>  
 <221> unsure  
 <222> (504)

<220>  
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 <222> (575)

<220>  
 <221> unsure  
 <222> (530)

<220>  
 <221> unsure  
 <222> (551)

<220>  
 <221> unsure  
 <222> (556)

<220>  
 <221> unsure  
 <222> (564)

<400> 37  
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 gtgtttggata tgtactccgt accacaacac ttgtttactc aagtttgtgt tattgttgac 120  
 aagctgggga aactgagtan ggaagaaatt gagaaggaat tgatttcaac tgggctgtca 180  
 tctgaagcag tacagggcac cattgaagtgt ctctctctca agtcactgtc caaacttgaa 240  
 gaggtgctag gctcaggtgt tgaagccggt gctgacttga agaacctctt ctgccttgct 300  
 gagcaaatatg gttattctga ttggatctgt ttgatgcat ctgttgttcg tggccttgca 360  
 tactacacan gggattgttt ttgaggcttt tgatagggaa gggaaactga nancatttgt 420  
 ggtggggggg aggtatgaca ggctacgtca acatttggaa ctgaagatnt ccaccctgtg 480  
 nctttggatt tggaatcctg tcanagtga ctcnnaaaga aaggtctttn ctacctgcac 540  
 tcaaataata nattgntcca ttgncaagac ttggggg 577

<210> 38  
 <211> 46  
 <212> PRT  
 <213> Triticum sp.

<220>  
 <221> UNSURE  
 <222> (38)

<400> 38  
 Ile Arg Leu Ser Ser Arg Lys Val Leu Gln Ala Val Leu Asp Met Tyr  
 1 5 10 15  
 Ser Val Pro Gln His Leu Phe Thr Gln Val Cys Val Ile Val Asp Lys  
 20 25 30

Leu Gly Lys Leu Ser Xaa Glu Glu Ile Glu Lys Glu Leu Ile  
35 40 45